

SEQUENCE LISTING

<110> DAICEL CHEMICAL INDUSTRIES, LTD.

<120> NOVEL ENONE REDUCTASES, METHODS FOR PRODUCING SAME, AND METHODS FOR SELECTIVELY REDUCING A CARBON-CARBON DOUBLE BOND OF AN α , β -UNSATURATED KETONE USING THE REDUCTASES

<130> D1-A0103

<140>

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<150> JP 2001-049363

<151> 2001-02-23

<160> 29

<170> PatentIn Ver. 2.1

<210> 1

<211> 1113

<212> DNA

<213> Kluyveromyces lactis

<220>

<221> CDS

<222> (1).. (1113)

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gct gtt gtt aaa aca gat gtc tca gtt cca gaa tta aag gag ggt aca 96
Ala Val Val Lys Thr Asp Val Ser Val Pro Glu Leu Lys Glu Gly Thr

20	25	30	
gcc ttg gtg aag gtt gag gct gtt gct ggt aac cca act gat tgg aag			144
Ala Leu Val Lys Val Glu Ala Val Ala Gly Asn Pro Thr Asp Trp Lys			
35	40	45	
cat att gct tat aag att ggt cca gaa ggt tca att cta gga tgt gac			192
His Ile Ala Tyr Lys Ile Gly Pro Glu Gly Ser Ile Leu Gly Cys Asp			
50	55	60	
att gct ggt aca gtt gtc aaa ctt gga cca aat gct agt act gac ttg			240
Ile Ala Gly Thr Val Val Lys Leu Gly Pro Asn Ala Ser Thr Asp Leu			
65	70	75	80
aag gtt gga gat acc ggt ttc ggt ttt gtt cac ggt gct tcc caa aca			288
Lys Val Gly Asp Thr Gly Phe Gly Phe Val His Gly Ala Ser Gln Thr			
85	90	95	
gat cct aaa aat ggt gca ttt gct gaa tat gcc agg gtt tat cca cct			336
Asp Pro Lys Asn Gly Ala Phe Ala Glu Tyr Ala Arg Val Tyr Pro Pro			
100	105	110	
ttg ttt tac aag agt aac tta act cac tca act gct gat gaa att tct			384
Leu Phe Tyr Lys Ser Asn Leu Thr His Ser Thr Ala Asp Glu Ile Ser			
115	120	125	
gaa ggc cct gtg aag aac ttc gaa tct gct gca tca ttg cca gtt tcg			432
Glu Gly Pro Val Lys Asn Phe Glu Ser Ala Ala Ser Leu Pro Val Ser			
130	135	140	
ttg aca act gct ggt gtt agt ttg tgt cat cac ttg ggc tca aaa atg			480
Leu Thr Thr Ala Gly Val Ser Leu Cys His His Leu Gly Ser Lys Met			
145	150	155	160
gaa tgg cac cca tct acc ccg caa cat act cat cca tta ttg att tgg			528
Glu Trp His Pro Ser Thr Pro Gln His Thr His Pro Leu Leu Ile Trp			

165	170	175	
ggt ggt gct aca gca gtg ggt caa caa cta atc caa gtt gcc aaa cat			576
Gly Gly Ala Thr Ala Val Gly Gln Gln Leu Ile Gln Val Ala Lys His			
180	185	190	
atc aat gct tat act aag att gta act gtt gct tct aaa aag cat gaa			624
Ile Asn Ala Tyr Thr Lys Ile Val Thr Val Ala Ser Lys Lys His Glu			
195	200	205	
aag ctt tta aag tct tat ggt gct gat gat gtc ttt gac tat cat gat			672
Lys Leu Leu Lys Ser Tyr Gly Ala Asp Asp Val Phe Asp Tyr His Asp			
210	215	220	
gca ggc gtt att gag cag atc aaa tcg aag tat cca aac ctg caa cat			720
Ala Gly Val Ile Glu Gln Ile Lys Ser Lys Tyr Pro Asn Leu Gln His			
225	230	235	240
gtt att gac gct gtg gga agc gaa gat agt atc ccc gag gcc tat aaa			768
Val Ile Asp Ala Val Gly Ser Glu Asp Ser Ile Pro Glu Ala Tyr Lys			
245	250	255	
gtc aca gca gat agt cta cct gcc aca tta tta gaa gtg gtt cca atg			816
Val Thr Ala Asp Ser Leu Pro Ala Thr Leu Leu Glu Val Val Pro Met			
260	265	270	
acc att gaa agc att cct gaa gaa atc aga aaa gat aat gtt aaa att			864
Thr Ile Glu Ser Ile Pro Glu Glu Ile Arg Lys Asp Asn Val Lys Ile			
275	280	285	
gat att act ttg ttg tat cgt gca tct ggt caa gaa att cta ttg ggt			912
Asp Ile Thr Leu Leu Tyr Arg Ala Ser Gly Gln Glu Ile Leu Leu Gly			
290	295	300	
gca aca aga ttt cct gct agt cca gaa tat cat gaa gcc aca gtt aaa			960
Ala Thr Arg Phe Pro Ala Ser Pro Glu Tyr His Glu Ala Thr Val Lys			

305 310 315 320

ttc gtt aag ttt ata aat cca cac ctt aac aac ggt gat atc cat cat 1008

Phe Val Lys Phe Ile Asn Pro His Leu Asn Asn Gly Asp Ile His His

325 330 335

atg aat att aaa gtt ttc agc aac ggc tta gat gat gtc cca gct ctc 1056

Met Asn Ile Lys Val Phe Ser Asn Gly Leu Asp Asp Val Pro Ala Leu

340 345 350

act gaa ggt ata aaa gaa ggt aaa aac aaa aat gtt aag tat gtt gcc 1104

Thr Glu Gly Ile Lys Glu Gly Lys Asn Lys Asn Val Lys Tyr Val Ala

355 360 365

agg tta taa 1113

Arg Leu

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<211> 370

<212> PRT

<213> Kluyveromyces lactis

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Ala Val Val Lys Thr Asp Val Ser Val Pro Glu Leu Lys Glu Gly Thr

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Ala Leu Val Lys Val Glu Ala Val Ala Gly Asn Pro Thr Asp Trp Lys

35 40 45

His Ile Ala Tyr Lys Ile Gly Pro Glu Gly Ser Ile Leu Gly Cys Asp

50 55 60

Ile Ala Gly Thr Val Val Lys Leu Gly Pro Asn Ala Ser Thr Asp Leu

65 70 75 80

Lys Val Gly Asp Thr Gly Phe Gly Phe Val His Gly Ala Ser Gln Thr

	85	90	95
Asp Pro Lys Asn Gly Ala Phe Ala Glu Tyr Ala Arg Val Tyr Pro Pro			
100	105	110	
Leu Phe Tyr Lys Ser Asn Leu Thr His Ser Thr Ala Asp Glu Ile Ser			
115	120	125	
Glu Gly Pro Val Lys Asn Phe Glu Ser Ala Ala Ser Leu Pro Val Ser			
130	135	140	
Leu Thr Thr Ala Gly Val Ser Leu Cys His His Leu Gly Ser Lys Met			
145	150	155	160
Glu Trp His Pro Ser Thr Pro Gln His Thr His Pro Leu Leu Ile Trp			
165	170	175	
Gly Gly Ala Thr Ala Val Gly Gln Gln Leu Ile Gln Val Ala Lys His			
180	185	190	
Ile Asn Ala Tyr Thr Lys Ile Val Thr Val Ala Ser Lys Lys His Glu			
195	200	205	
Lys Leu Leu Lys Ser Tyr Gly Ala Asp Asp Val Phe Asp Tyr His Asp			
210	215	220	
Ala Gly Val Ile Glu Gln Ile Lys Ser Lys Tyr Pro Asn Leu Gln His			
225	230	235	240
Val Ile Asp Ala Val Gly Ser Glu Asp Ser Ile Pro Glu Ala Tyr Lys			
245	250	255	
Val Thr Ala Asp Ser Leu Pro Ala Thr Leu Leu Glu Val Val Pro Met			
260	265	270	
Thr Ile Glu Ser Ile Pro Glu Glu Ile Arg Lys Asp Asn Val Lys Ile			
275	280	285	
Asp Ile Thr Leu Leu Tyr Arg Ala Ser Gly Gln Glu Ile Leu Leu Gly			
290	295	300	
Ala Thr Arg Phe Pro Ala Ser Pro Glu Tyr His Glu Ala Thr Val Lys			
305	310	315	320
Phe Val Lys Phe Ile Asn Pro His Leu Asn Asn Gly Asp Ile His His			
325	330	335	
Met Asn Ile Lys Val Phe Ser Asn Gly Leu Asp Asp Val Pro Ala Leu			
340	345	350	
Thr Glu Gly Ile Lys Glu Gly Lys Asn Lys Asn Val Lys Tyr Val Ala			
355	360	365	
Arg Leu			

370

<210> 3

<211> 1145

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (6).. (1136)

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aat ggc aag gct gta gtc aaa cag gac att cca att cct gaa tta gaa 98

Asn Gly Lys Ala Val Val Lys Gln Asp Ile Pro Ile Pro Glu Leu Glu

20

25

30

gaa gga ttt gtt cta att aag act gtc gcc gtt gcc ggt aac cct acc 146

Glu Gly Phe Val Leu Ile Lys Thr Val Ala Val Ala Gly Asn Pro Thr

35

40

45

gat tgg aaa cat att gat ttc aag att ggt cct caa ggt gcc ctc tta 194

Asp Trp Lys His Ile Asp Phe Lys Ile Gly Pro Gln Gly Ala Leu Leu

50

55

60

ggc tgt gat gca gcc ggc caa atc gta aag ttg ggc cca aat gtt gat 242

Gly Cys Asp Ala Ala Gly Gln Ile Val Lys Leu Gly Pro Asn Val Asp

65

70

75

gct gca cgc ttt gcc att ggt gat tac att tat ggg gtt att cac ggt 290

Ala Ala Arg Phe Ala Ile Gly Asp Tyr Ile Tyr Gly Val Ile His Gly

80	85	90	95	
gct tca gtg agg ttc ccc tca aac ggt gcc ttt gct gag tac tct gcc				338
Ala Ser Val Arg Phe Pro Ser Asn Gly Ala Phe Ala Glu Tyr Ser Ala				
100		105	110	
att tca tcc gag act gct tat aaa cca gcc aga gag ttt aga ttg tgc				386
Ile Ser Ser Glu Thr Ala Tyr Lys Pro Ala Arg Glu Phe Arg Leu Cys				
115		120	125	
ggt aaa gac aag cta cca gaa ggc ccc gta aaa tct tta gaa ggg gca				434
Gly Lys Asp Lys Leu Pro Glu Gly Pro Val Lys Ser Leu Glu Gly Ala				
130		135	140	
gta tcc ctc cca gtc tca ttg acc acg gct ggt atg atc ctt aca cat				482
Val Ser Leu Pro Val Ser Leu Thr Thr Ala Gly Met Ile Leu Thr His				
145		150	155	
agt ttt ggc ttg gac atg aca tgg aag ccc tcc aaa gcg caa aga gat				530
Ser Phe Gly Leu Asp Met Thr Trp Lys Pro Ser Lys Ala Gln Arg Asp				
160	165	170	175	
caa ccc atc tta ttt tgg ggt ggt gcc act gct gtt ggc cag atg ctt				578
Gln Pro Ile Leu Phe Trp Gly Gly Ala Thr Ala Val Gly Gln Met Leu				
180		185	190	
att caa ttg gca aaa aaa cta aac ggt ttc agc aag atc atc gtc gtt				626
Ile Gln Leu Ala Lys Lys Leu Asn Gly Phe Ser Lys Ile Ile Val Val				
195		200	205	
gct tct cgt aaa cat gaa aaa ttg ttg aaa gag tac ggt gca gat gaa				674
Ala Ser Arg Lys His Glu Lys Leu Leu Lys Glu Tyr Gly Ala Asp Glu				
210		215	220	
ctt ttt gac tac cac gat gct gac gtt atc gaa cag ata aaa aag aag				722
Leu Phe Asp Tyr His Asp Ala Asp Val Ile Glu Gln Ile Lys Lys Lys				

225	230	235	
tac aac aac att cct tac ttg gtg gac tgt gtc tcc aac aca gaa act 770			
Tyr Asn Asn Ile Pro Tyr Leu Val Asp Cys Val Ser Asn Thr Glu Thr			
240	245	250	255
att caa cag gtg tac aaa tgt gcc gct gat gac tta gac gct acg gtc 818			
Ile Gln Gln Val Tyr Lys Cys Ala Ala Asp Asp Leu Asp Ala Thr Val			
	260	265	270
gtt caa ttg acc gtt tta acc gaa aaa gat atc aag gag gaa gac agg 866			
Val Gln Leu Thr Val Leu Thr Glu Lys Asp Ile Lys Glu Glu Asp Arg			
	275	280	285
agg caa aac gtc agt att gaa gga acc ctt cta tat ttg ata gga ggt 914			
Arg Gln Asn Val Ser Ile Glu Gly Thr Leu Leu Tyr Leu Ile Gly Gly			
	290	295	300
aac gac gtc cca ttt ggc acg ttt act ttg cca gca gac cct gaa tac 962			
Asn Asp Val Pro Phe Gly Thr Phe Thr Leu Pro Ala Asp Pro Glu Tyr			
	305	310	315
aag gaa gcc gcc ata aaa ttt att aag ttc atc aat cca aaa atc aat 1010			
Lys Glu Ala Ala Ile Lys Phe Ile Lys Phe Ile Asn Pro Lys Ile Asn			
320	325	330	335
gat ggt gaa atc cac cac atc cca gtg aaa gtt tac aag aac ggg tta 1058			
Asp Gly Glu Ile His His Ile Pro Val Lys Val Tyr Lys Asn Gly Leu			
	340	345	350
gat gat atc cca cag tta ctt gat gat att aag cac ggg agg aat tct 1106			
Asp Asp Ile Pro Gln Leu Leu Asp Asp Ile Lys His Gly Arg Asn Ser			
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375

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<211> 376

<212> PRT

<213> *Saccharomyces cerevisiae*

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 20 25 30
 Gly Phe Val Leu Ile Lys Thr Val Ala Val Ala Gly Asn Pro Thr Asp
 35 40 45
 Trp Lys His Ile Asp Phe Lys Ile Gly Pro Gln Gly Ala Leu Leu Gly
 50 55 60
 Cys Asp Ala Ala Gly Gln Ile Val Lys Leu Gly Pro Asn Val Asp Ala
 65 70 75 80
 Ala Arg Phe Ala Ile Gly Asp Tyr Ile Tyr Gly Val Ile His Gly Ala
 85 90 95
 Ser Val Arg Phe Pro Ser Asn Gly Ala Phe Ala Glu Tyr Ser Ala Ile
 100 105 110
 Ser Ser Glu Thr Ala Tyr Lys Pro Ala Arg Glu Phe Arg Leu Cys Gly
 115 120 125
 Lys Asp Lys Leu Pro Glu Gly Pro Val Lys Ser Leu Glu Gly Ala Val
 130 135 140
 Ser Leu Pro Val Ser Leu Thr Thr Ala Gly Met Ile Leu Thr His Ser
 145 150 155 160
 Phe Gly Leu Asp Met Thr Trp Lys Pro Ser Lys Ala Gln Arg Asp Gln
 165 170 175
 Pro Ile Leu Phe Trp Gly Gly Ala Thr Ala Val Gly Gln Met Leu Ile
 180 185 190
 Gln Leu Ala Lys Lys Leu Asn Gly Phe Ser Lys Ile Ile Val Val Ala
 195 200 205
 Ser Arg Lys His Glu Lys Leu Leu Lys Glu Tyr Gly Ala Asp Glu Leu

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210	215	220
Phe Asp Tyr His Asp Ala Asp Val Ile Glu Gln Ile Lys Lys Lys Tyr		
225	230	235
Asn Asn Ile Pro Tyr Leu Val Asp Cys Val Ser Asn Thr Glu Thr Ile		240
	245	250
Gln Gln Val Tyr Lys Cys Ala Ala Asp Asp Leu Asp Ala Thr Val Val		255
	260	265
Gln Leu Thr Val Leu Thr Glu Lys Asp Ile Lys Glu Glu Asp Arg Arg		270
	275	280
Gln Asn Val Ser Ile Glu Gly Thr Leu Leu Tyr Leu Ile Gly Gly Asn		285
	290	295
Asp Val Pro Phe Gly Thr Phe Thr Leu Pro Ala Asp Pro Glu Tyr Lys		300
305	310	315
Glu Ala Ala Ile Lys Phe Ile Lys Phe Ile Asn Pro Lys Ile Asn Asp		320
	325	330
Gly Glu Ile His His Ile Pro Val Lys Val Tyr Lys Asn Gly Leu Asp		335
	340	345
Asp Ile Pro Gln Leu Leu Asp Asp Ile Lys His Gly Arg Asn Ser Gly		350
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Glu Lys Leu Val Ala Val Leu Lys		365
	370	375

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<222> (1).. (1134)

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gac ggt aaa gcg gtt gtt aaa gag ggc att ccc att cct gaa ttg gaa				96
Asp Gly Lys Ala Val Val Lys Glu Gly Ile Pro Ile Pro Glu Leu Glu				
20		25	30	
gaa gga ttc gta ttg att aag aca ctc gct gtt gct ggt aac ccc act				144
Glu Gly Phe Val Leu Ile Lys Thr Leu Ala Val Ala Gly Asn Pro Thr				
35		40	45	
gat tgg gca cac att gac tac aag atc ggg cct caa gga tct att ctg				192
Asp Trp Ala His Ile Asp Tyr Lys Ile Gly Pro Gln Gly Ser Ile Leu				
50		55	60	
gga tgt gat gct gct ggc caa att gtc aaa ttg ggc cca gct gtc aat				240
Gly Cys Asp Ala Ala Gly Gln Ile Val Lys Leu Gly Pro Ala Val Asn				
65		70	75	80
cct aaa gac ttt tct atc ggt gat tat att tat ggg ttc att cac gga				288
Pro Lys Asp Phe Ser Ile Gly Asp Tyr Ile Tyr Gly Phe Ile His Gly				
85		90	95	
tct tcc gta agg ttt cct tcc aat ggt gct ttt gct gaa tat tct gct				336
Ser Ser Val Arg Phe Pro Ser Asn Gly Ala Phe Ala Glu Tyr Ser Ala				
100		105	110	
att tca act gtg gtt gcc tac aaa tca ccc aat gaa ctc aaa ttt ttg				384
Ile Ser Thr Val Val Ala Tyr Lys Ser Pro Asn Glu Leu Lys Phe Leu				
115		120	125	
ggt gag gat gtt cta cct gcc ggc cct gtc agg tct ttg gaa ggt gta				432
Gly Glu Asp Val Leu Pro Ala Gly Pro Val Arg Ser Leu Glu Gly Val				
130		135	140	
gcc act atc cca gtg tca ctg acc aca gcc ggc ttg gtg ttg acc tat				480
Ala Thr Ile Pro Val Ser Leu Thr Thr Ala Gly Leu Val Leu Thr Tyr				

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145	150	155	160	
aac ttg ggc ttg gac ctg aag tgg gag cca tca acc cca caa aga aaa				528
Asn Leu Gly Leu Asp Leu Lys Trp Glu Pro Ser Thr Pro Gln Arg Lys				
	165	170	175	
ggc ccc atc tta tta tgg ggc ggt gca act gca gta ggt cag tcg ctc				576
Gly Pro Ile Leu Leu Trp Gly Gly Ala Thr Ala Val Gly Gln Ser Leu				
	180	185	190	
atc caa tta gcc aat aaa ttg aat ggc ttc acc aag atc att gtt gtg				624
Ile Gln Leu Ala Asn Lys Leu Asn Gly Phe Thr Lys Ile Ile Val Val				
	195	200	205	
gct tct egg aag cac gaa aaa ctt ttg aaa gaa tat ggt gct gat gaa				672
Ala Ser Arg Lys His Glu Lys Leu Leu Lys Glu Tyr Gly Ala Asp Glu				
	210	215	220	
tta ttt gat tat cat gat att gac gtg gta gaa caa att aaa cac aag				720
Leu Phe Asp Tyr His Asp Ile Asp Val Val Glu Gln Ile Lys His Lys				
225	230	235	240	
tac aac aat atc tcg tat tta gtc gac tgt gtc gcg aat caa gat acg				768
Tyr Asn Asn Ile Ser Tyr Leu Val Asp Cys Val Ala Asn Gln Asp Thr				
	245	250	255	
ctt caa caa gtg tac aaa tgt gcg gcc gat aaa cag gat gct aca att				816
Leu Gln Gln Val Tyr Lys Cys Ala Ala Asp Lys Gln Asp Ala Thr Ile				
	260	265	270	
gtt gaa tta aaa aat ttg aca gaa gaa aac gtc aaa aaa gag aac agg				864
Val Glu Leu Lys Asn Leu Thr Glu Glu Asn Val Lys Lys Glu Asn Arg				
	275	280	285	
aga caa aac gtt act att gac ata ata agg cta tat tca ata ggt ggc				912
Arg Gln Asn Val Thr Ile Asp Ile Ile Arg Leu Tyr Ser Ile Gly Gly				

290

295

300

cat gaa gta cca ttt gga aac att act tta cca gcc gac tca gaa gct 960
 His Glu Val Pro Phe Gly Asn Ile Thr Leu Pro Ala Asp Ser Glu Ala
 305 310 315 320

agg aaa gct gca ata aaa ttt atc aaa ttc atc aat cca aag att aat 1008
 Arg Lys Ala Ala Ile Lys Phe Ile Lys Phe Ile Asn Pro Lys Ile Asn
 325 330 335

gat gga caa att cgc cat att cca gta agg gtc tat aag aac ggg ctt 1056
 Asp Gly Gln Ile Arg His Ile Pro Val Arg Val Tyr Lys Asn Gly Leu
 340 345 350

tgt gat gtt cct cat atc cta aaa gac atc aaa tat ggt aag aac tct 1104
 Cys Asp Val Pro His Ile Leu Lys Asp Ile Lys Tyr Gly Lys Asn Ser
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ggt gaa aaa ctc gtt gcc gta tta aac taa 1134
 Gly Glu Lys Leu Val Ala Val Leu Asn
 370 375

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<211> 377

<212> PRT

<213> *Saccharomyces cerevisiae*

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 Glu Gly Phe Val Leu Ile Lys Thr Leu Ala Val Ala Gly Asn Pro Thr
 35 40 45
 Asp Trp Ala His Ile Asp Tyr Lys Ile Gly Pro Gln Gly Ser Ile Leu

50	55	60
Gly Cys Asp Ala Ala Gly Gln Ile Val Lys Leu Gly Pro Ala Val Asn		
65	70	75
Pro Lys Asp Phe Ser Ile Gly Asp Tyr Ile Tyr Gly Phe Ile His Gly		80
	85	90
Ser Ser Val Arg Phe Pro Ser Asn Gly Ala Phe Ala Glu Tyr Ser Ala		95
100	105	110
Ile Ser Thr Val Val Ala Tyr Lys Ser Pro Asn Glu Leu Lys Phe Leu		
115	120	125
Gly Glu Asp Val Leu Pro Ala Gly Pro Val Arg Ser Leu Glu Gly Val		
130	135	140
Ala Thr Ile Pro Val Ser Leu Thr Thr Ala Gly Leu Val Leu Thr Tyr		
145	150	155
Asn Leu Gly Leu Asp Leu Lys Trp Glu Pro Ser Thr Pro Gln Arg Lys		160
	165	170
Gly Pro Ile Leu Leu Trp Gly Gly Ala Thr Ala Val Gly Gln Ser Leu		175
180	185	190
Ile Gln Leu Ala Asn Lys Leu Asn Gly Phe Thr Lys Ile Ile Val Val		
195	200	205
Ala Ser Arg Lys His Glu Lys Leu Leu Lys Glu Tyr Gly Ala Asp Glu		
210	215	220
Leu Phe Asp Tyr His Asp Ile Asp Val Val Glu Gln Ile Lys His Lys		
225	230	235
Tyr Asn Asn Ile Ser Tyr Leu Val Asp Cys Val Ala Asn Gln Asp Thr		240
	245	250
Leu Gln Gln Val Tyr Lys Cys Ala Ala Asp Lys Gln Asp Ala Thr Ile		255
260	265	270
Val Glu Leu Lys Asn Leu Thr Glu Glu Asn Val Lys Lys Glu Asn Arg		
275	280	285
Arg Gln Asn Val Thr Ile Asp Ile Ile Arg Leu Tyr Ser Ile Gly Gly		
290	295	300
His Glu Val Pro Phe Gly Asn Ile Thr Leu Pro Ala Asp Ser Glu Ala		
305	310	315
Arg Lys Ala Ala Ile Lys Phe Ile Lys Phe Ile Asn Pro Lys Ile Asn		320
	325	330
Asp Gly Gln Ile Arg His Ile Pro Val Arg Val Tyr Lys Asn Gly Leu		335

340 345 350
 Cys Asp Val Pro His Ile Leu Lys Asp Ile Lys Tyr Gly Lys Asn Ser
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 Gly Glu Lys Leu Val Ala Val Leu Asn
 370 375

<210> 7

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<212> DNA

<213> *Saccharomyces cerevisiae*

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<221> CDS

<222> (7).. (1113)

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gag ggc gtt ccc att cct gaa ttg gaa gaa gga ttc gta ttg att aag 96

Glu Gly Val Pro Ile Pro Glu Leu Glu Glu Gly Phe Val Leu Ile Lys

15

20

25

30

aca ctc gct gtt gct ggt aac ccg act gat tgg gca cac att gac tac 144

Thr Leu Ala Val Ala Gly Asn Pro Thr Asp Trp Ala His Ile Asp Tyr

35

40

45

aag gtc ggg cct caa gga tct att ctg gga tgt gac gct gcc ggc caa 192

Lys Val Gly Pro Gln Gly Ser Ile Leu Gly Cys Asp Ala Ala Gly Gln

50

55

60

att gtc aaa ttg ggc cca gcc gtc gat cct aaa gac ttt tct att ggt 240

Ile Val Lys Leu Gly Pro Ala Val Asp Pro Lys Asp Phe Ser Ile Gly

65	70	75	
gat tat att tat ggg ttc att cac gga tct tcc gta agg ttt cct tcc			288
Asp Tyr Ile Tyr Gly Phe Ile His Gly Ser Ser Val Arg Phe Pro Ser			
80	85	90	
aat ggt gct ttt gct gaa tat tct gct att tca act gtg gtt gcc tac			336
Asn Gly Ala Phe Ala Glu Tyr Ser Ala Ile Ser Thr Val Val Ala Tyr			
95	100	105	110
aaa tca ccc aat gaa ctc aaa ttt ttg ggt gaa gat gtt cta cct gcc			384
Lys Ser Pro Asn Glu Leu Lys Phe Leu Gly Glu Asp Val Leu Pro Ala			
115	120	125	
ggc cct gtc agg tct ttg gaa ggg gca gcc act atc cca gtg tca ctg			432
Gly Pro Val Arg Ser Leu Glu Gly Ala Ala Thr Ile Pro Val Ser Leu			
130	135	140	
acc aca gct ggc ttg gtg ttg acc tat aac ttg ggc ttg aac ctg aag			480
Thr Thr Ala Gly Leu Val Leu Thr Tyr Asn Leu Gly Leu Asn Leu Lys			
145	150	155	
tgg gag cca tca acc cca caa aga aac ggc ccc atc tta tta tgg ggc			528
Trp Glu Pro Ser Thr Pro Gln Arg Asn Gly Pro Ile Leu Leu Trp Gly			
160	165	170	
ggt gca act gca gta ggt cag tcg ctc atc caa tta gcc aat aaa ttg			576
Gly Ala Thr Ala Val Gly Gln Ser Leu Ile Gln Leu Ala Asn Lys Leu			
175	180	185	190
aat ggc ttc acc aag atc att gtt gtg gct tct cgg aaa cac gaa aaa			624
Asn Gly Phe Thr Lys Ile Ile Val Val Ala Ser Arg Lys His Glu Lys			
195	200	205	
ctg ttg aaa gaa tat ggt gct gat caa cta ttt gat tac cat gat att			672
Leu Leu Lys Glu Tyr Gly Ala Asp Gln Leu Phe Asp Tyr His Asp Ile			

210	215	220	
gac gtg gta gaa caa att aaa cac aag tac aac aat atc tcg tat tta			720
Asp Val Val Glu Gln Ile Lys His Lys Tyr Asn Asn Ile Ser Tyr Leu			
225	230	235	
gtc gac tgt gtc gcg aat caa aat acg ctt caa caa gtg tac aaa tgt			768
Val Asp Cys Val Ala Asn Gln Asn Thr Leu Gln Gln Val Tyr Lys Cys			
240	245	250	
gcg gcc gat aaa cag gat gct acc gtt gtc gaa tta act aat ttg aca			816
Ala Ala Asp Lys Gln Asp Ala Thr Val Val Glu Leu Thr Asn Leu Thr			
255	260	265	270
gaa gaa aac gtc aaa aag gag aat agg agg caa aat gtc act att gac			864
Glu Glu Asn Val Lys Lys Glu Asn Arg Arg Gln Asn Val Thr Ile Asp			
275	280	285	
aga aca aga ctg tat tca ata ggc ggc cat gaa gta cca ttt ggt ggc			912
Arg Thr Arg Leu Tyr Ser Ile Gly Gly His Glu Val Pro Phe Gly Gly			
290	295	300	
att act ttc cct gct gac cca gaa gcc agg aga gct gcc acc gaa ttc			960
Ile Thr Phe Pro Ala Asp Pro Glu Ala Arg Arg Ala Ala Thr Glu Phe			
305	310	315	
gtc aag ttc atc aat cca aag att agt gat ggg caa att cac cat att			1008
Val Lys Phe Ile Asn Pro Lys Ile Ser Asp Gly Gln Ile His His Ile			
320	325	330	
cca gca agg gtc tat aag aac ggg ctt tac gat gtt cct cgt atc ctg			1056
Pro Ala Arg Val Tyr Lys Asn Gly Leu Tyr Asp Val Pro Arg Ile Leu			
335	340	345	350
gaa gac att aaa atc ggt aag aac tct ggt gaa aaa ctc gtt gcc gta			1104
Glu Asp Ile Lys Ile Gly Lys Asn Ser Gly Glu Lys Leu Val Ala Val			

355

360

365

tta aac taa tctagaaac

1122

Leu Asn

<210> 8

<211> 368

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 8

Met Lys Ala Val Val Ile Glu Asp Gly Lys Ala Val Val Lys Glu Gly

1

5

10

15

Val Pro Ile Pro Glu Leu Glu Glu Gly Phe Val Leu Ile Lys Thr Leu

20

25

30

Ala Val Ala Gly Asn Pro Thr Asp Trp Ala His Ile Asp Tyr Lys Val

35

40

45

Gly Pro Gln Gly Ser Ile Leu Gly Cys Asp Ala Ala Gly Gln Ile Val

50

55

60

Lys Leu Gly Pro Ala Val Asp Pro Lys Asp Phe Ser Ile Gly Asp Tyr

65

70

75

80

Ile Tyr Gly Phe Ile His Gly Ser Ser Val Arg Phe Pro Ser Asn Gly

85

90

95

Ala Phe Ala Glu Tyr Ser Ala Ile Ser Thr Val Val Ala Tyr Lys Ser

100

105

110

Pro Asn Glu Leu Lys Phe Leu Gly Glu Asp Val Leu Pro Ala Gly Pro

115

120

125

Val Arg Ser Leu Glu Gly Ala Ala Thr Ile Pro Val Ser Leu Thr Thr

130

135

140

Ala Gly Leu Val Leu Thr Tyr Asn Leu Gly Leu Asn Leu Lys Trp Glu

145

150

155

160

Pro Ser Thr Pro Gln Arg Asn Gly Pro Ile Leu Leu Trp Gly Gly Ala

165

170

175

Thr Ala Val Gly Gln Ser Leu Ile Gln Leu Ala Asn Lys Leu Asn Gly

180

185

190

Phe Thr Lys Ile Ile Val Val Ala Ser Arg Lys His Glu Lys Leu Leu
 195 200 205
 Lys Glu Tyr Gly Ala Asp Gln Leu Phe Asp Tyr His Asp Ile Asp Val
 210 215 220
 Val Glu Gln Ile Lys His Lys Tyr Asn Asn Ile Ser Tyr Leu Val Asp
 225 230 235 240
 Cys Val Ala Asn Gln Asn Thr Leu Gln Gln Val Tyr Lys Cys Ala Ala
 245 250 255
 Asp Lys Gln Asp Ala Thr Val Val Glu Leu Thr Asn Leu Thr Glu Glu
 260 265 270
 Asn Val Lys Lys Glu Asn Arg Arg Gln Asn Val Thr Ile Asp Arg Thr
 275 280 285
 Arg Leu Tyr Ser Ile Gly Gly His Glu Val Pro Phe Gly Gly Ile Thr
 290 295 300
 Phe Pro Ala Asp Pro Glu Ala Arg Arg Ala Ala Thr Glu Phe Val Lys
 305 310 315 320
 Phe Ile Asn Pro Lys Ile Ser Asp Gly Gln Ile His His Ile Pro Ala
 325 330 335
 Arg Val Tyr Lys Asn Gly Leu Tyr Asp Val Pro Arg Ile Leu Glu Asp
 340 345 350
 Ile Lys Ile Gly Lys Asn Ser Gly Glu Lys Leu Val Ala Val Leu Asn
 355 360 365

<210> 9

<211> 12

<212> PRT

<213> Kluyveromyces lactis

<400> 9

Ser Tyr Gly Ala Asp Asp Val Phe Asp Tyr His Asp

1

5

10

<210> 10

<211> 12

<212> PRT

<213> Kluyveromyces lactis

<400> 10

Ile Gly Pro Glu Gly Ser Ile Leu Gly Cys Asp Ile

1

5

10

<210> 11

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<220>

<221> misc_feature

<222> (12)

<223> n indicates g, a, c or t.

<400> 11

tgrtartcra anacrtertc

20

<210> 12

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<220>

<221> misc_feature

<222> (18)

<223> n indicates g, a, c or t.

<400> 12

atwgghccwg argghtcnat

20

<210> 13

<211> 20

<212> DNA

<213> Artificial Sequence

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synthesized primer sequence

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<222> (9)

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<400> 13

atwgghccng argghagyat

20

<210> 14

<211> 509

<212> DNA

<213> Kluyveromyces lactis

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ccaaatgcta gtactgactt gaaggttgga gataccgggtt tcggttttgc tccaggtgct 120
tcccaaacag atcctaataa tgggtgcattt gctgaatatg ccagggttta tccacctttg 180

ttttacaaga gtaacttaac tcaactcaact gctgatgaaa tttctgaagg cctgtgaag 240
 aacttcgaat ctgctgcac attgccagtt tcgttgacaa ctgctgggtgt tagtttgtgt 300
 catcacttgg gctcaaaaat ggaatggcac ccatctaccc cgcaacatac tcatccatta 360
 ttgatttggg gtggtgctac agcagtggtt caacaactaa tccaagttgc caaacatac 420
 aatgcttata ctaagattgt aactgttgct tctaaaaagc atgaaaagct tttaaagtct 480
 tatggtgctg atgacgtmtt cgactacca 509

<210> 15

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:an artificially
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<400> 15

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<210> 16

<211> 32

<212> DNA

<213> Artificial Sequence

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<400> 16

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<210> 17

<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:an artificially synthesized primer sequence

<400> 17

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21

<210> 18

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:an artificially synthesized primer sequence

<400> 18

tcatgaagcc acagttaa at tcg

23

<210> 19

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:an artificially synthesized primer sequence

<400> 19

atattcatat gatggat atc accg

24

<210> 20

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<400> 20

ctggaattct accatggctt cagttccaac cactcaaaaa g

41

<210> 21

<211> 39

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:an artificially
synthesized primer sequence

<400> 21

gacaagcttc tagattataa cctggcaaca tacttaaca

39

<210> 22

<211> 25

<212> DNA

<213> Artificial Sequence

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<400> 22

caaacatgtc tgcctcgatt ccaga

25

<210> 23

<211> 31

<212> DNA

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<400> 23

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31

<210> 24

<211> 32

<212> DNA

<213> Artificial Sequence

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synthesized primer sequence

<400> 24

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32

<210> 25

<211> 38

<212> DNA

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<400> 25

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38

<210> 26

<211> 27

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:an artificially
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<400> 26

gaaatcatga aagctgtcgt cattgaa

27

<210> 27

<211> 37

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:an artificially
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<400> 27

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37

<210> 28

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially synthesized primer sequence

<400> 28

tgtaaacga cggccagt

18

<210> 29

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:an artificially synthesized primer sequence

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caggaaacag ctatgacc

18